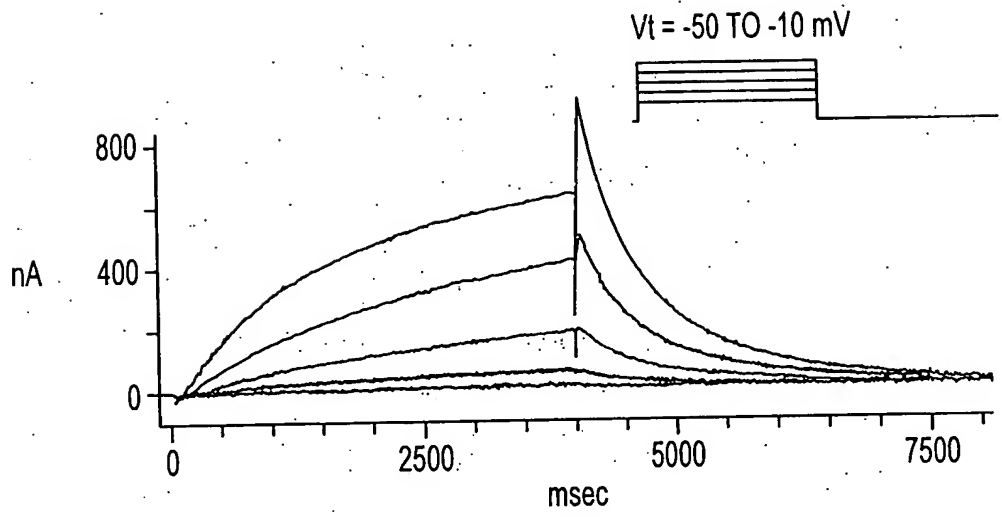
Vt = -50 TO -10 mV
800
400
0
nA
0
2500
5000
7500
msec

FIG. 1A

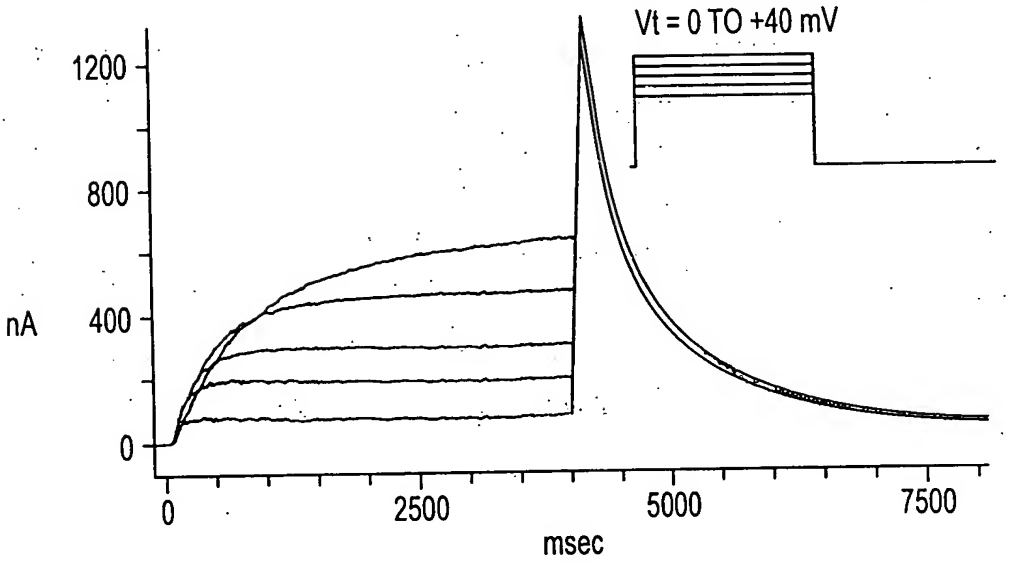
Vt = 0 TO +40 mV
1200
800
400
0
nA
0
2500
5000
7500
msec

FIG. 1B

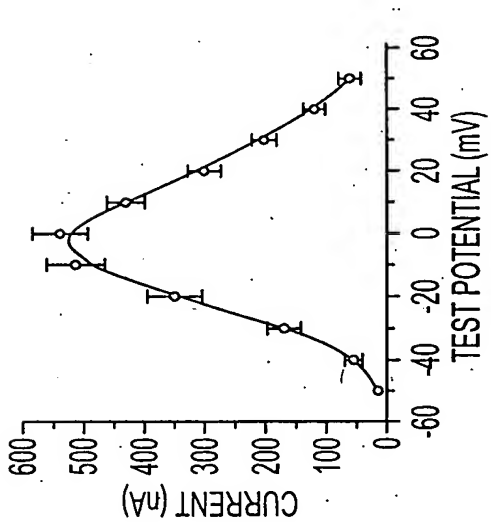

FIG. 1C

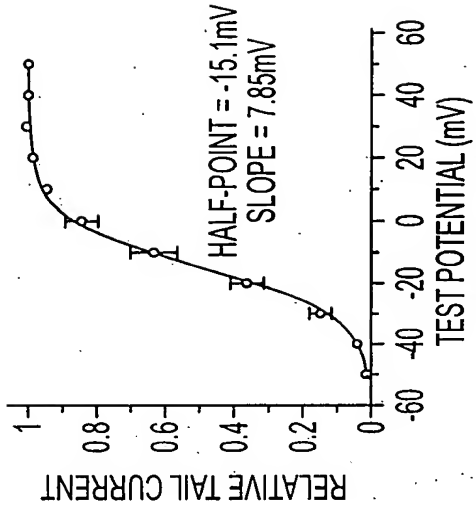

FIG. 1D

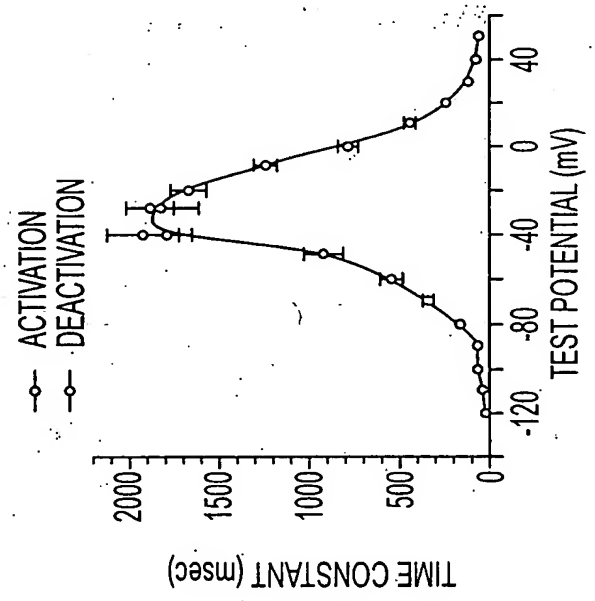

FIG. 2C

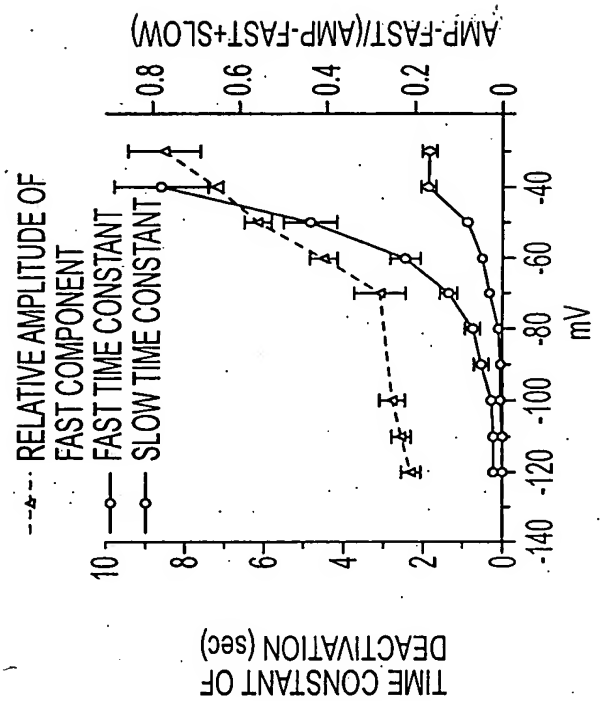

FIG. 2D

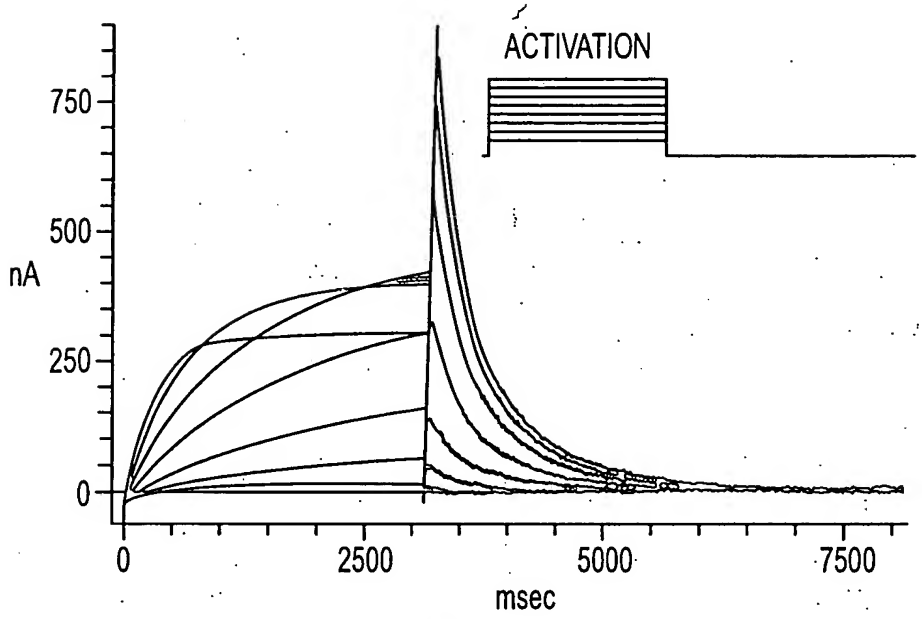
ACTIVATION
750
500
250
0
nA
0
2500
5000
7500
msec

FIG. 2A

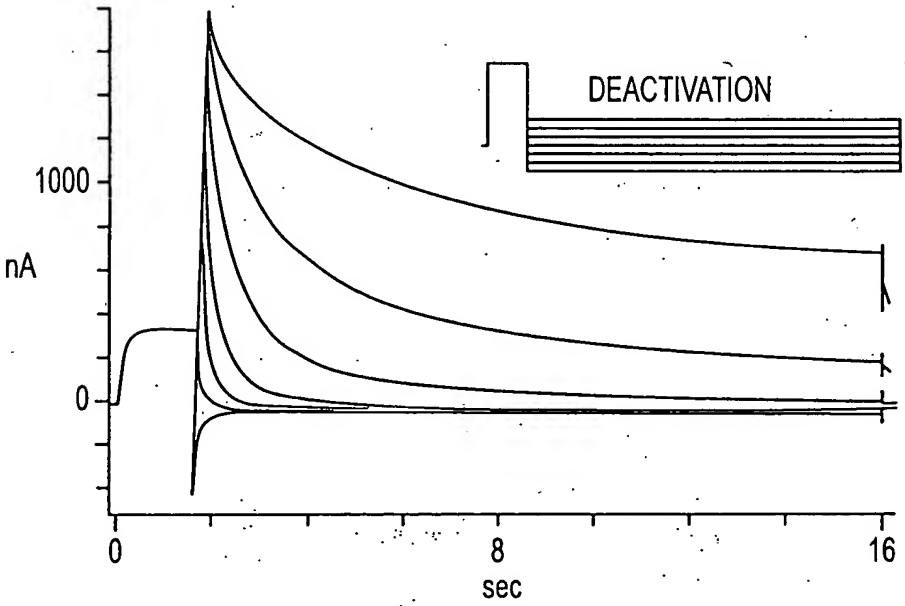
DEACTIVATION
1000
0
nA
0
8
16
sec

FIG. 2B

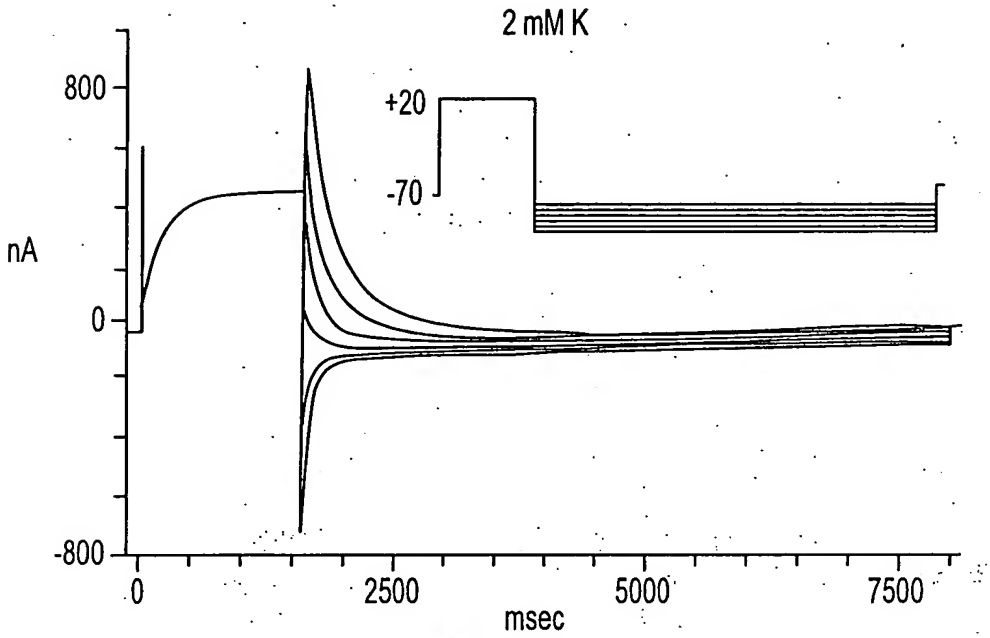

FIG. 3A

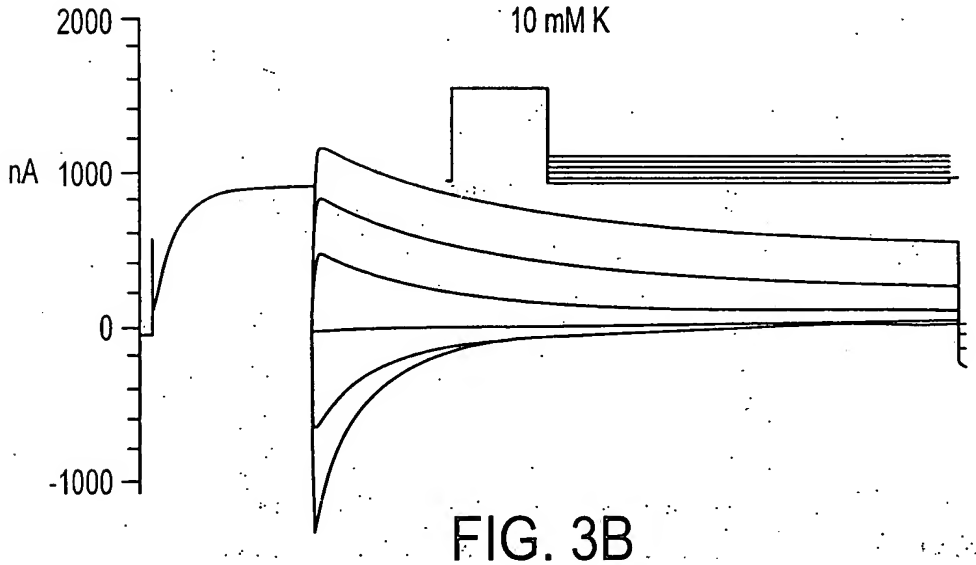

FIG. 3B

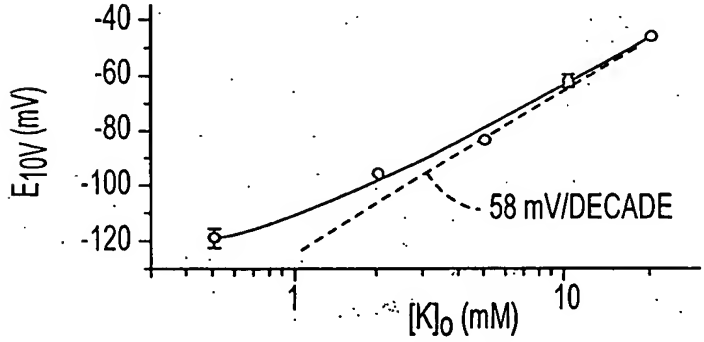

FIG. 3C

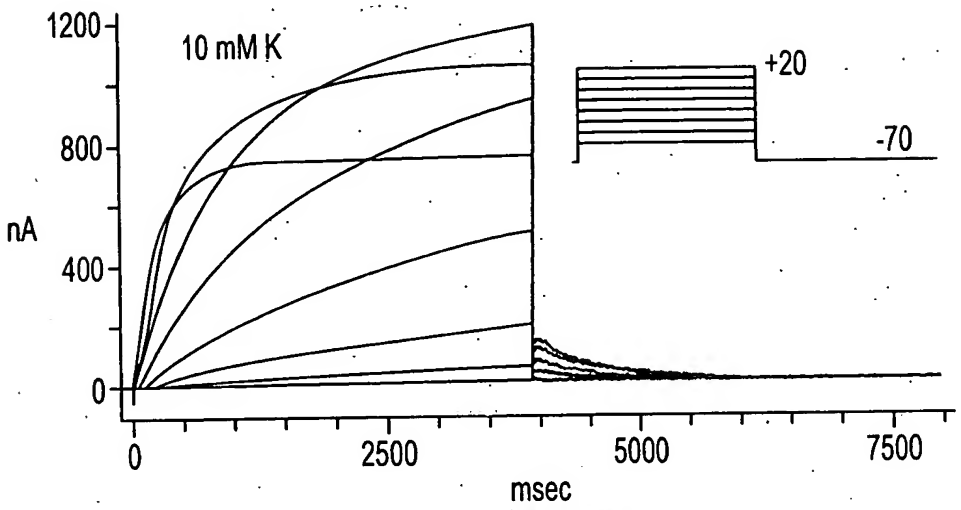

FIG. 4A

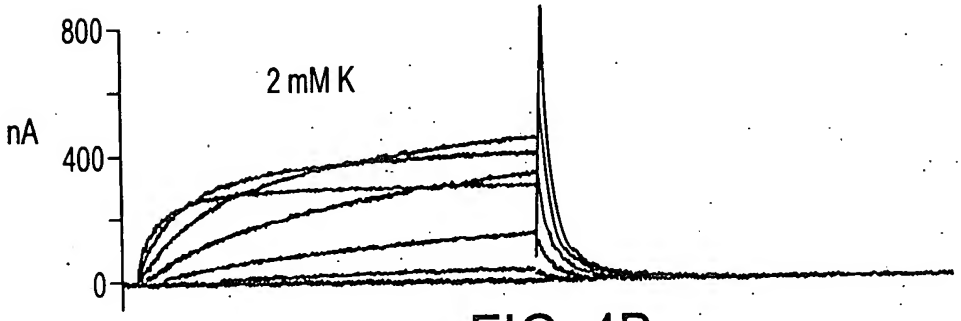

FIG. 4B

FIG. 4C

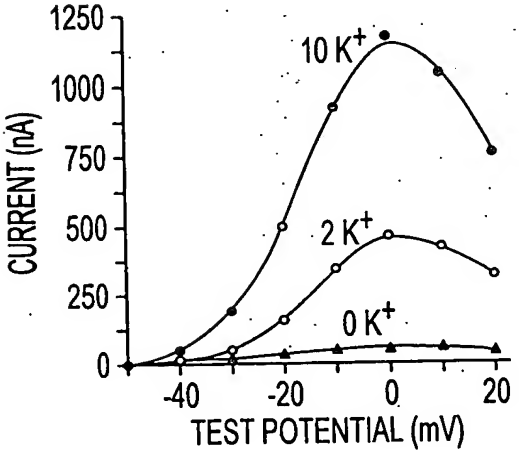

FIG. 4D

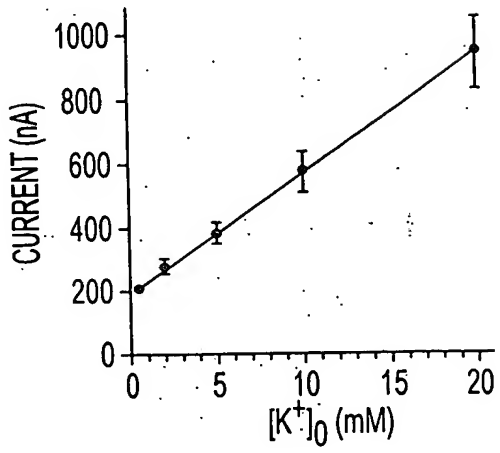

FIG. 4E

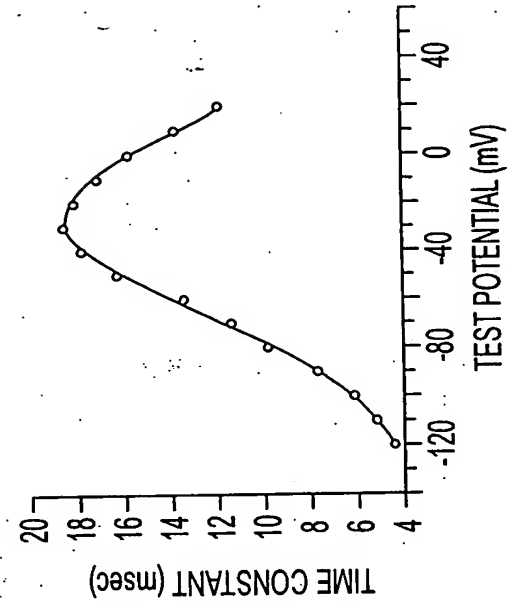
TIME CONSTANT (msec)
20
18
16
14
12
10
8
6
4
40
0
-40
-80
-120
TEST POTENTIAL (mV)

FIG. 5B

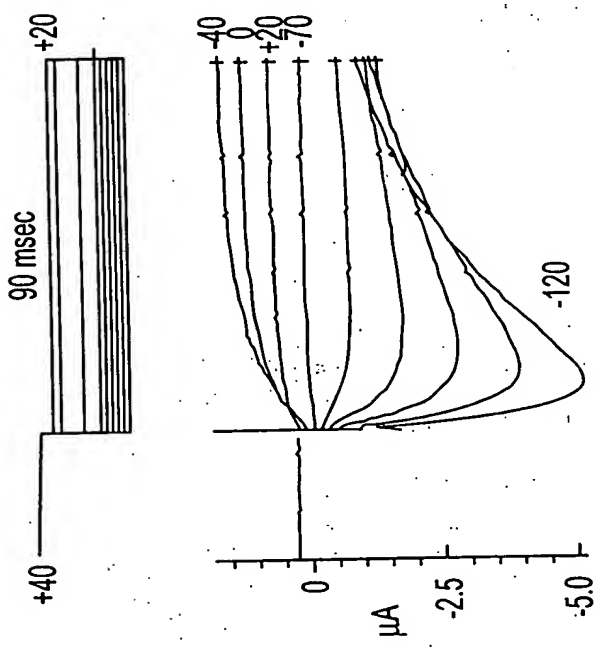
+20
90 msec
+40
-40
0
+20
-70
-120
0
-2.5
-5.0
μA

FIG. 5A

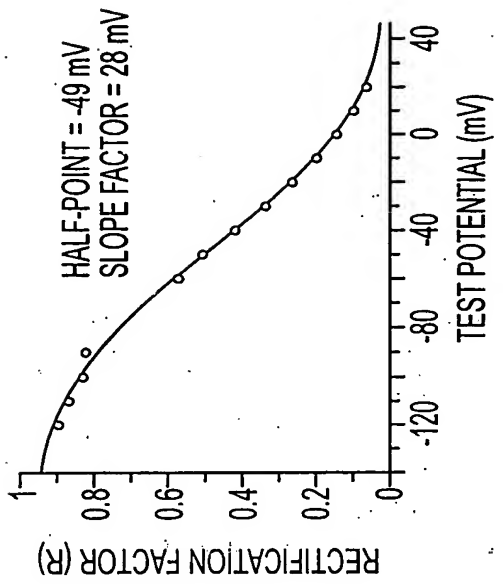
HALF-POINT = -49 mV
SLOPE FACTOR = 28 mV
RECTIFICATION FACTOR (R)
1
0.8
0.6
0.4
0.2
0
40
0
-40
-80
-120
TEST POTENTIAL (mV)

FIG. 5D

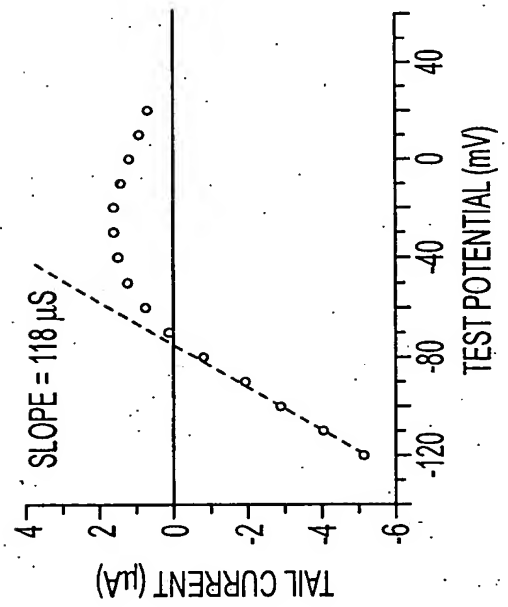
SLOPE = 118 µS
TAIL CURRENT (µA)
4
2
0
-2
-4
-6
40
0
-40
-80
-120
TEST POTENTIAL (mV)

FIG. 5C

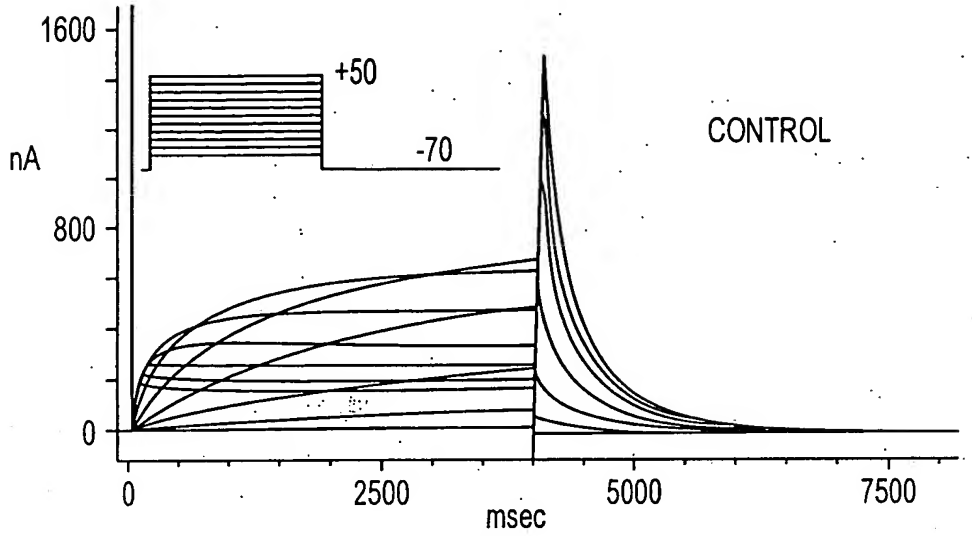

FIG. 6A

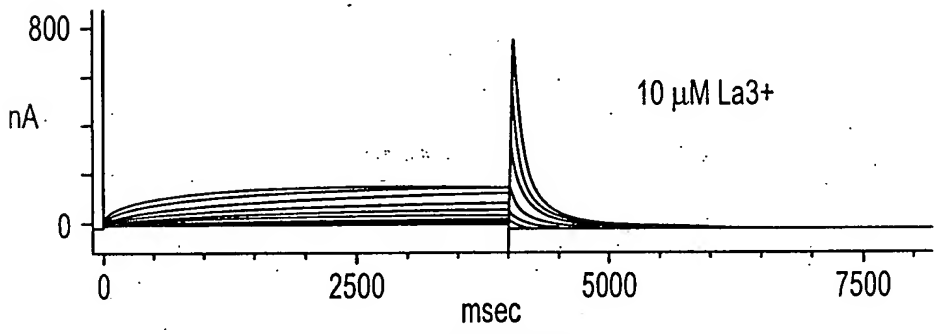

FIG. 6B

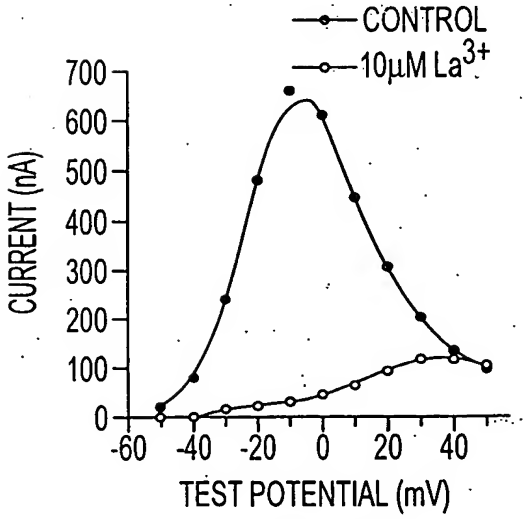

FIG. 6C

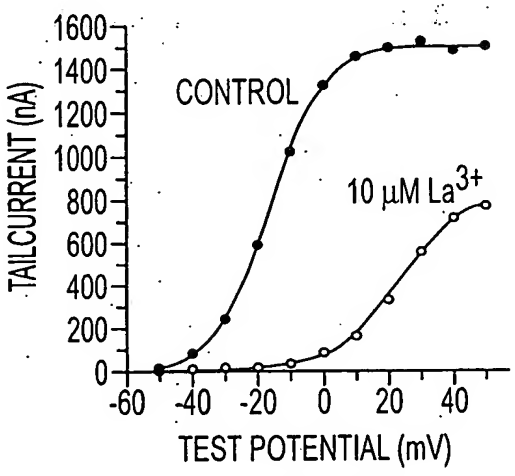

FIG. 6D

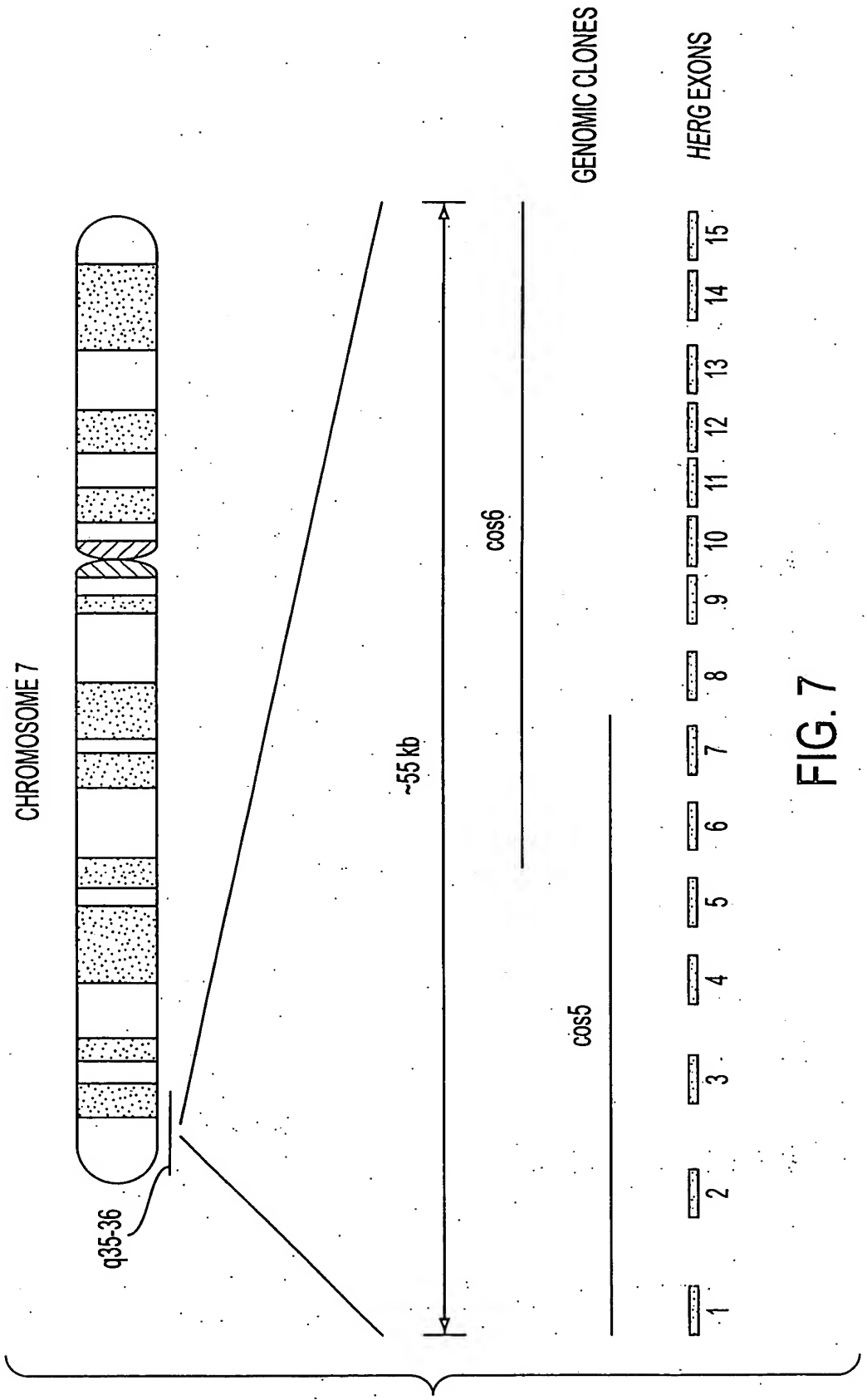
CHROMOSOME 7
q35-36
~55 kb
cos6
cos5
GENOMIC CLONES
HERG EXONS
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15

FIG. 7

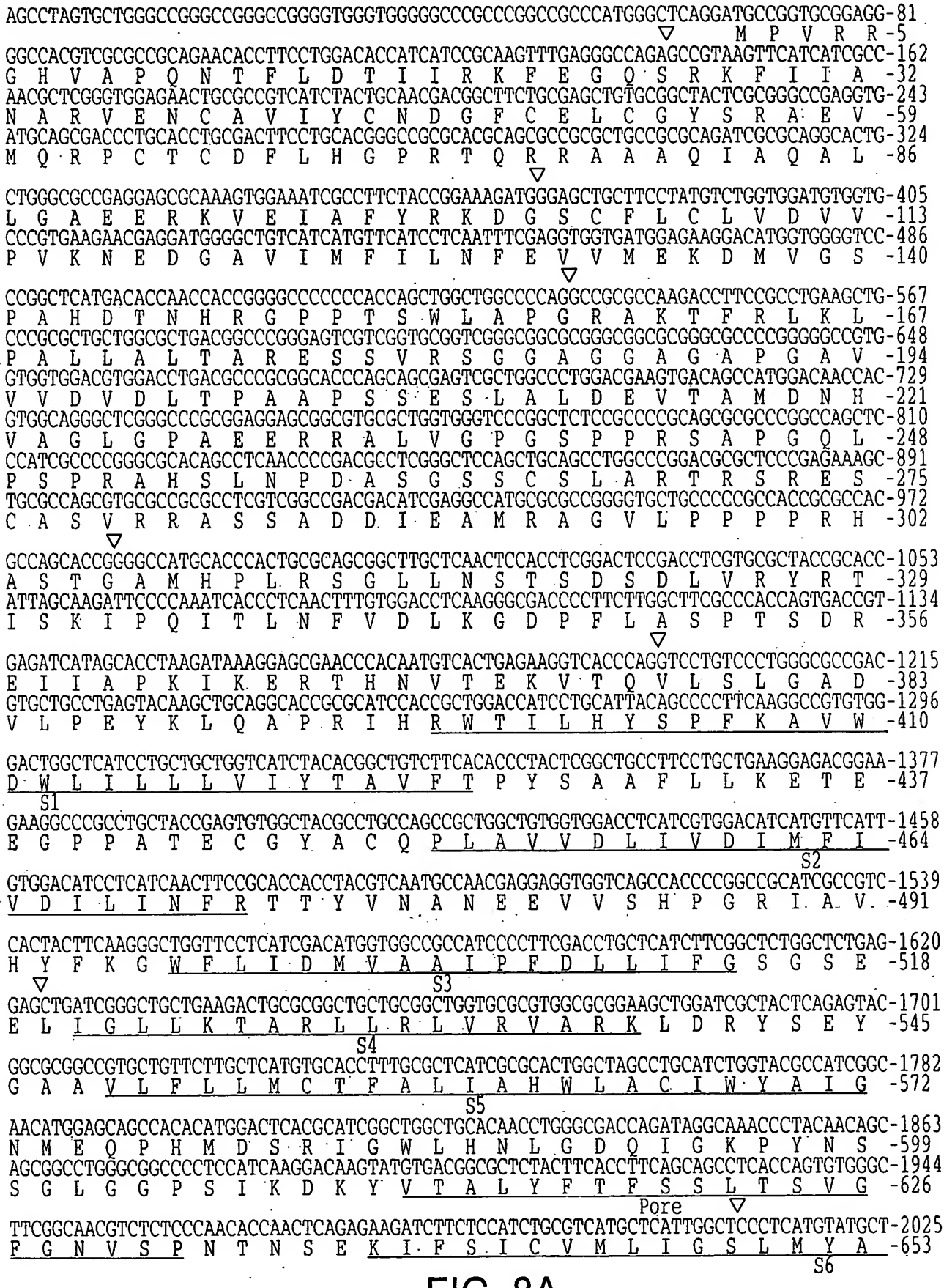

FIG. 8A

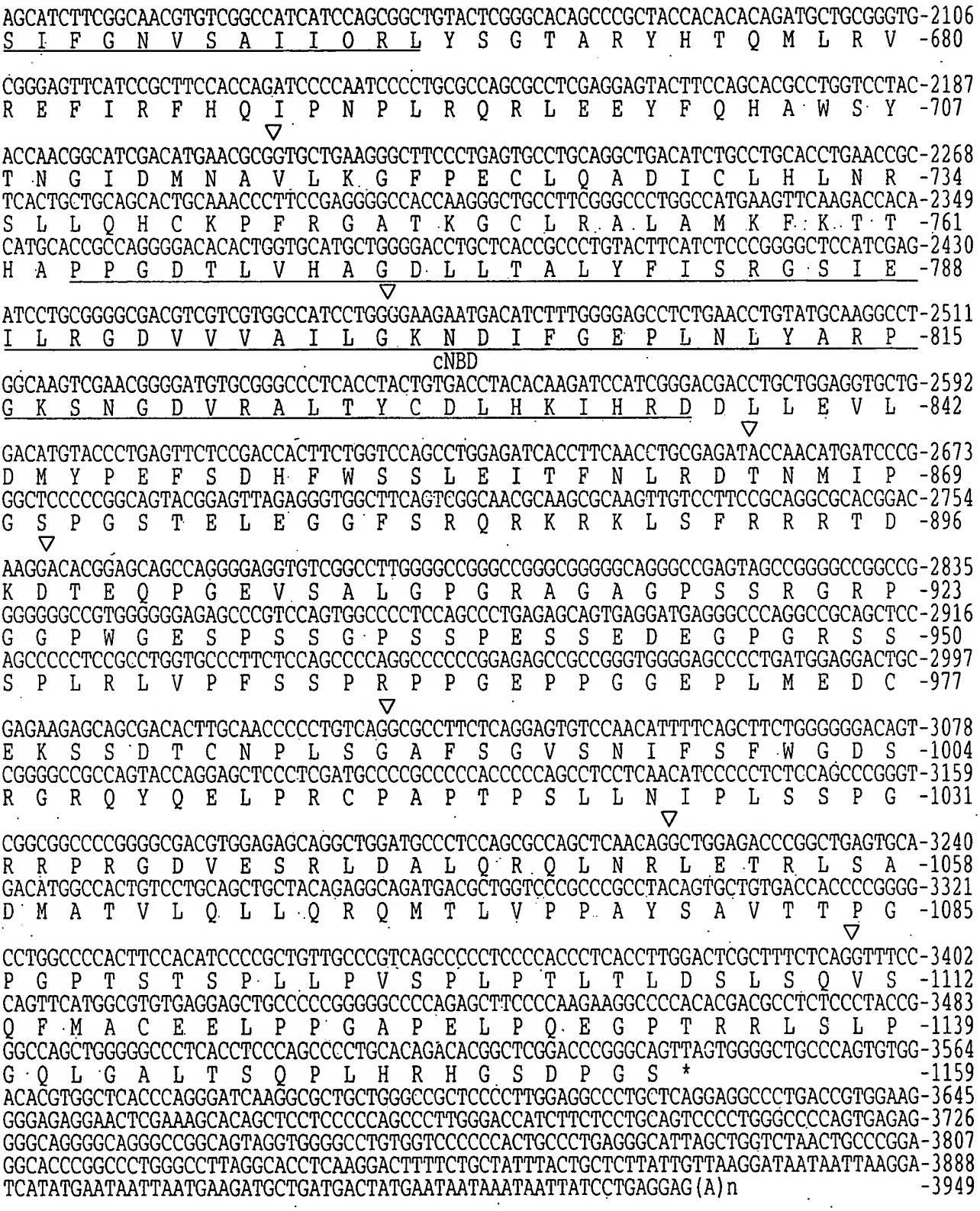
AGCATCTTCGGCAACGTGTCGGCCATCATCCAGCGGCTGTACTCGGGCACAGCCCGCTACCACACACAGATGCTGCGGGTG-2106
S I F G N V S A I I Q R L Y S G T A R Y H T Q M L R V -680
CGGGAGTTCATCCGCTTCCACCAGATCCCCAATCCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCCTGGTCCTAC-2187
R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707
ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268
T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734
TCACTGCTGCAGCACTGCAAACCCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCCCTGGCCATGAAGTTCAAGACCACA-2349
S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761
CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACCGCCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430
H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788
ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511
I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815
cNBD
GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592
G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842
GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673
D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869
GGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCCTTCCGCAGGCGCACGGAC-2754
G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896
AAGGACACGGAGCAGCCAGGGGAGGTGTCGGCCTTGGGGCCGGGCCGGGCGGGGGCAGGGCCGAGTAGCCGGGGCCGGCCG-2835
K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923
GGGGGGCCGTGGGGGGAGAGCCCGTCCAGTGGCCCCTCCAGCCCTGAGAGCAGTGAGGATGAGGGCCCAGGCCGCAGCTCC-2916
G G P W G E S P S S G P S S P E S S E D E G P G R S S -950
AGCCCCCTCCGCCTGGTGCCCTTCTCCAGCCCCAGGCCCCCCGGAGAGCCGCCGGGTGGGGAGCCCCTGATGGAGGACTGC-2997
S P L R L V P F S S P R P P G E P P G G E P L M E D C -977
GAGAAGAGCAGCGACACTTGCAACCCCCTGTCAGGCGCCTTCTCAGGAGTGTCCAACATTTTCAGCTTCTGGGGGGACAGT-3078
E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004
CGGGGCCGCCAGTACCAGGAGCTCCCTCGATGCCCCGCCCCCACCCCCAGCCTCCTCAACATCCCCCTCTCCAGCCCGGGT-3159
R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031
CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240
R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058
GACATGGCCACTGTCCTGCAGCTGCTACAGAGGCAGATGACGCTGGTCCCGCCCGCCTACAGTGCTGTGACCACCCCGGGG-3321
D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085
CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCCTCACCTTGGACTCGCTTTCTCAGGTTTCC-3402
P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112
CAGTTCATGGCGTGTGAGGAGCTGCCCCCGGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCCTCTCCCTACCG-3483
Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139
GGCCAGCTGGGGGCCCTCACCTCCCAGCCCCTGCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCCAGTGTGG-3564
G Q L G A L T S Q P L H R H G S D P G S * -1159
ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCCGCTCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645
GGGAGAGGAACTCGAAAGCACAGCTCCTCCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAGAG-3726
GGGCAGGGGCAGGGCCGGCAGTAGGTGGGGCCTGTGGTCCCCCCACTGCCCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807
GGCACCCGGCCCTGGGCCTTAGGCACCTCAAGGACTTTTCTGCTATTTACTGCTCTTATTGTTAAGGATAATAATTAAGGA-3888
TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAAATAATTATCCTGAGGAG(A)n -3949

FIG. 8B

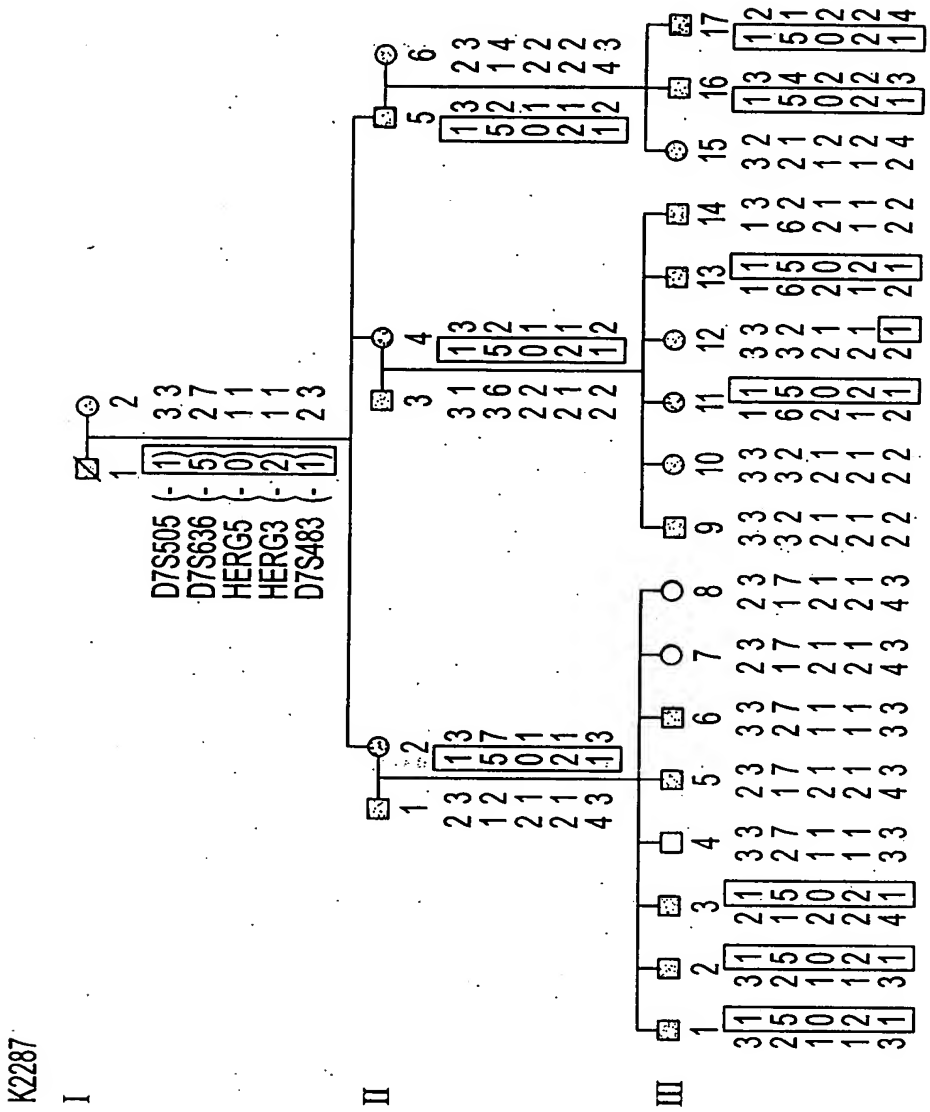
K2287
I
II
III
D7S505
D7S636
HERG5
HERG3
D7S483

FIG. 9B

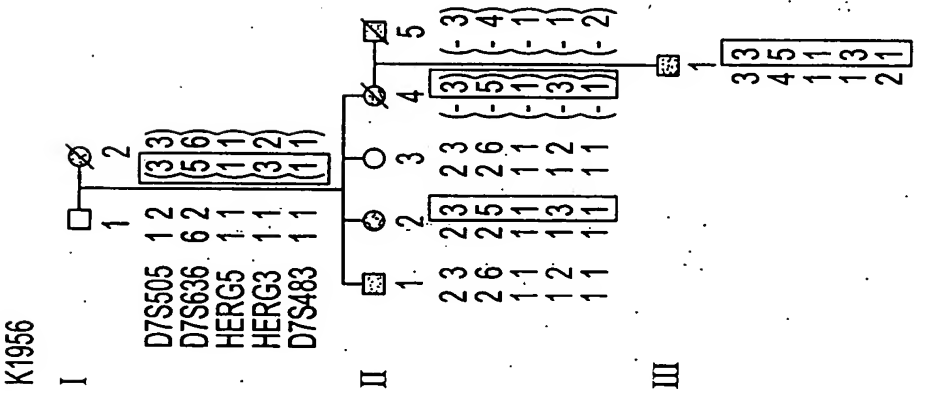
K1956
I
II
III
D7S505
D7S636
HERG5
HERG3
D7S483

FIG. 9A

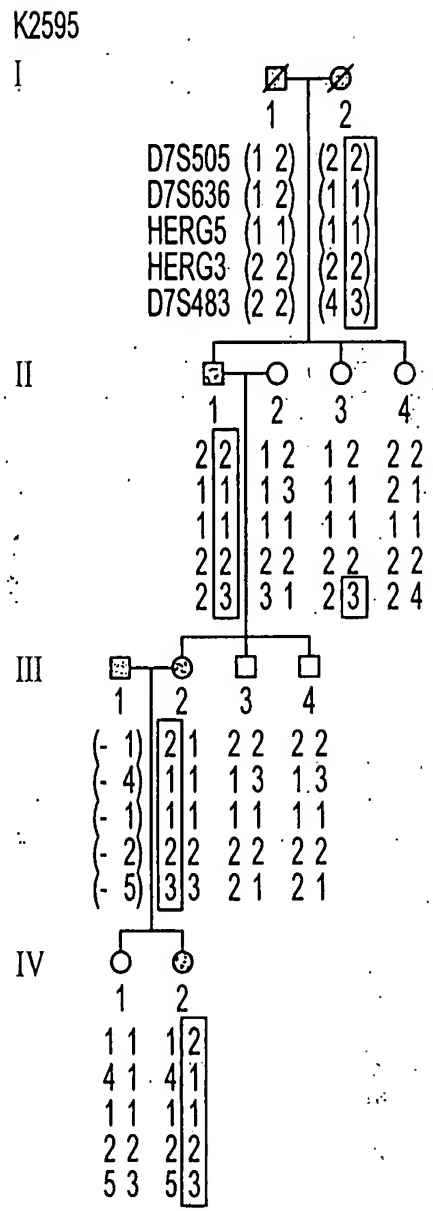

FIG. 9C

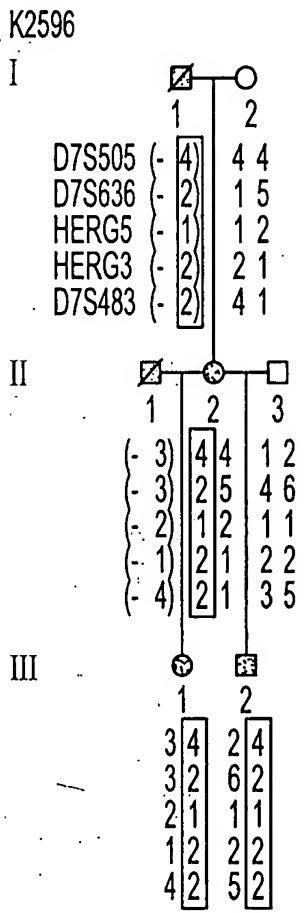

FIG. 9D

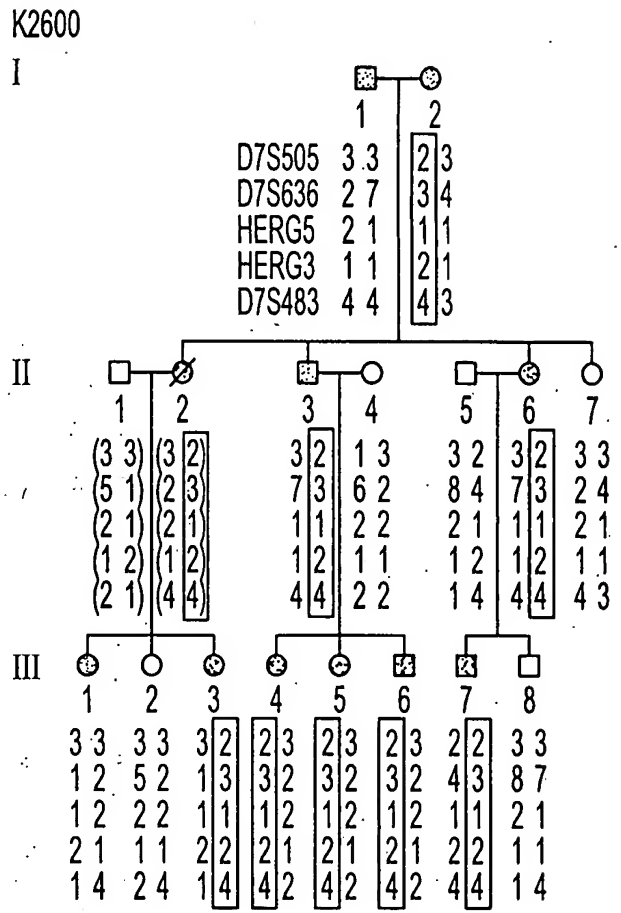

FIG. 9E

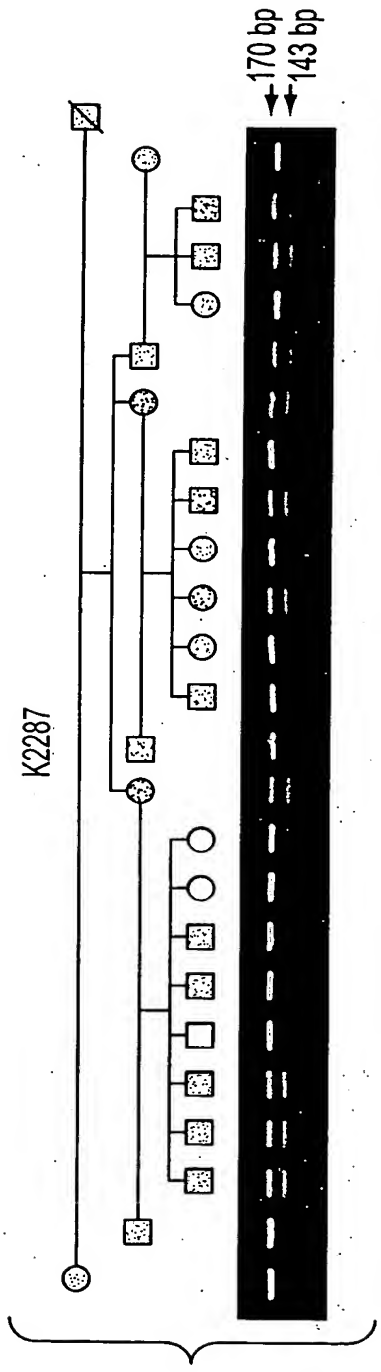

FIG. 10A

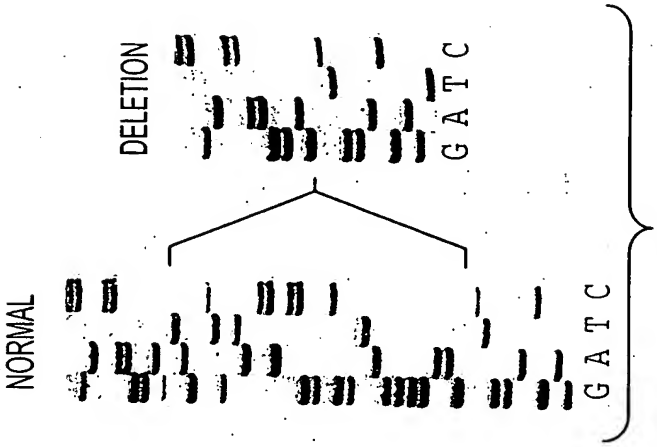

FIG. 10B

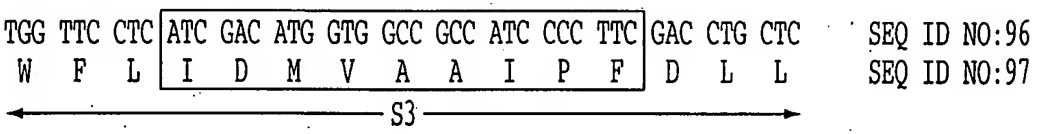

FIG. 10C

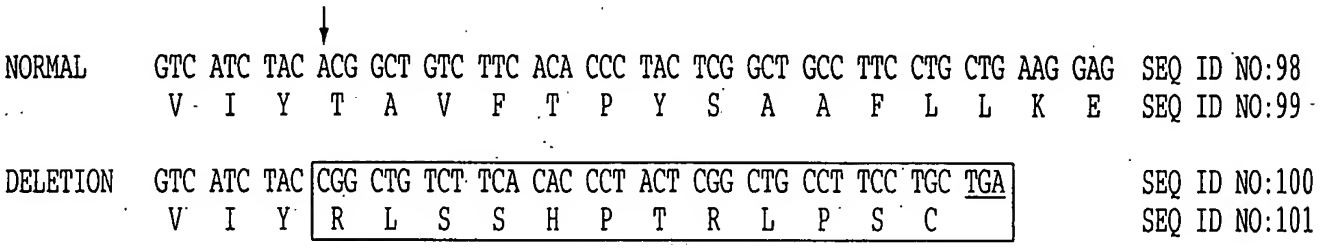

FIG. 11C

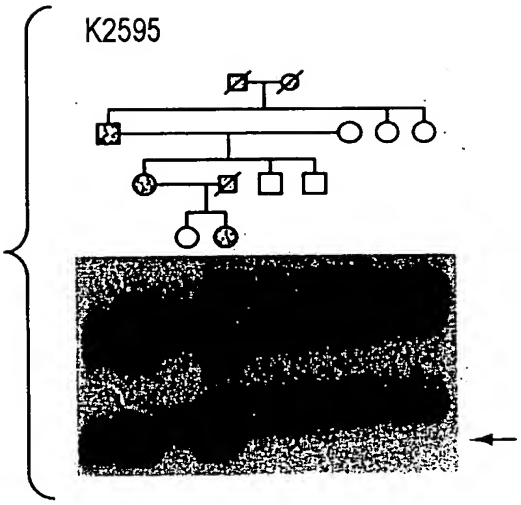

FIG. 11A

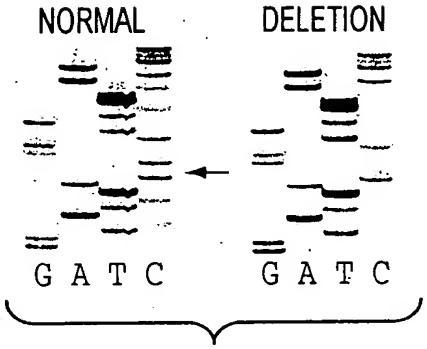

FIG. 11B

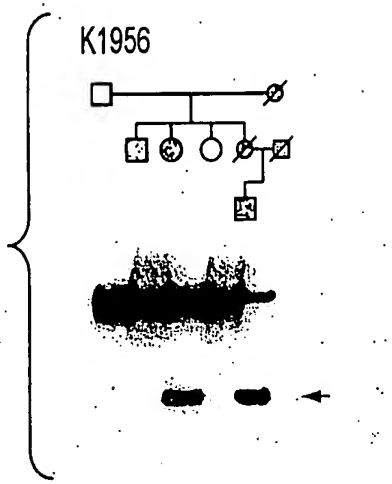

FIG. 12A

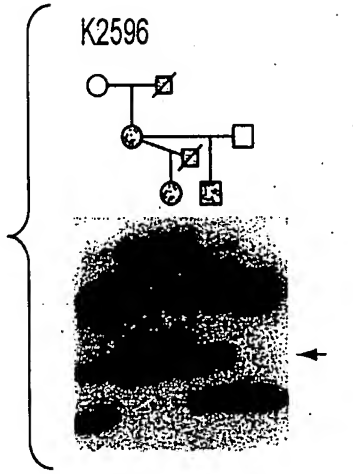

FIG. 12C

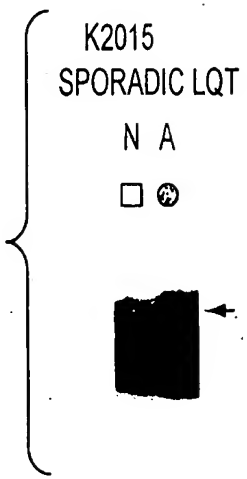

FIG. 12E

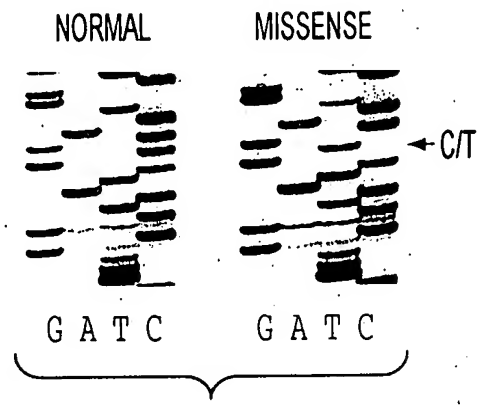

FIG. 12B

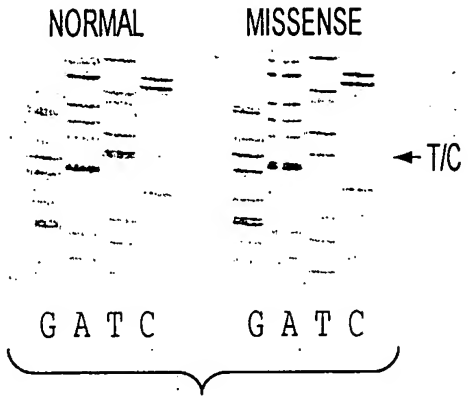

FIG. 12D

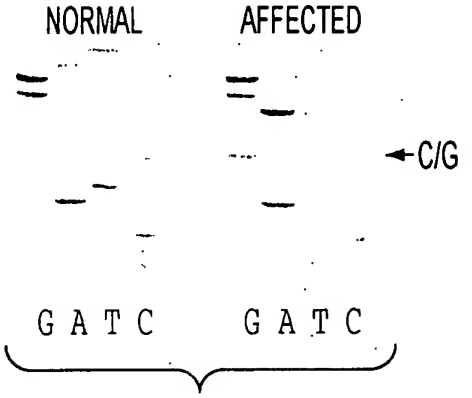

FIG. 12F

	GTG→V / GCG	SEQ ID NO:
	L I A H W L	102
	←S5→	
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

FIG. 12G

	GAC→D / AAC	SEQ ID NO:
	D I L I N F R	108
	←S2→	
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

FIG. 12H

C
↓
5'-CAT CCT GG // gtatggg-3'

FIG. 12I

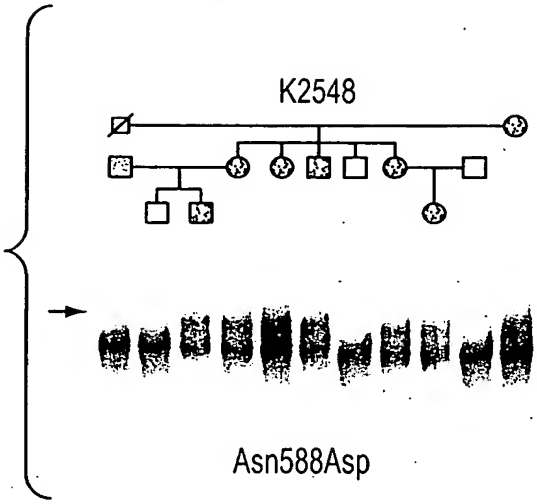

FIG. 13A

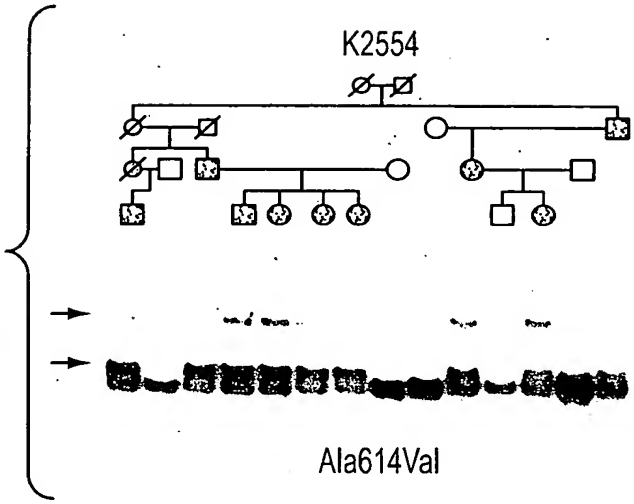

FIG. 13B

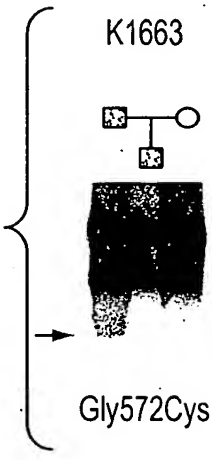

FIG. 13C

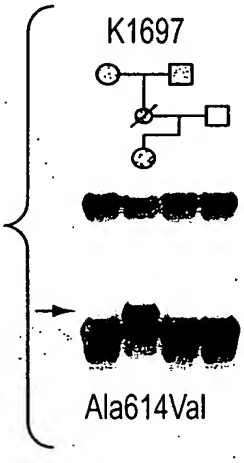

FIG. 13D

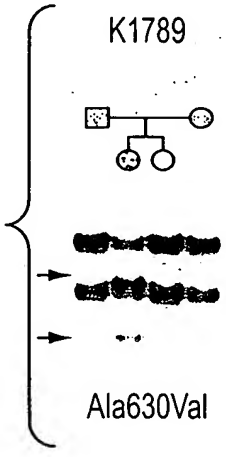

FIG. 13E

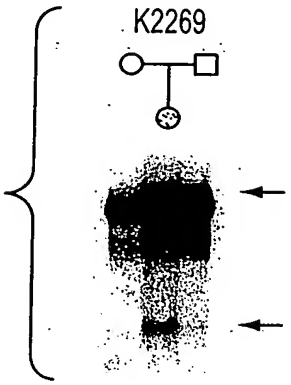

FIG. 14A

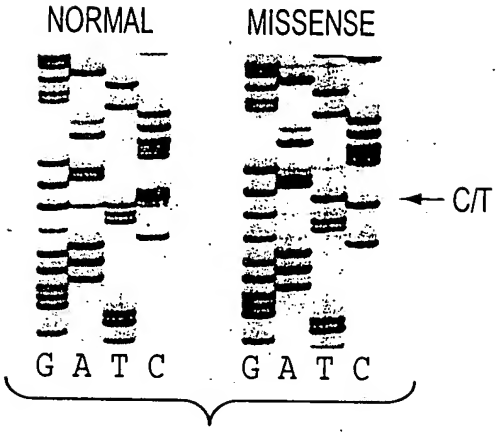

FIG. 14B

		SEQ ID NO:
	S V G F G N V S (AGC → S, GGC)	112
	← PORE →	
K2269	S V G F S N V S	113
H-Erg	S V G F G N V S	112
M-Eag	S V G F G N I A	114
R-Eag	S V G F G N I A	114
Eag	S V G F G N V A	115
Elk	S V G F G N V S	112
Shaker	T V G Y G D M T	116

FIG. 14C

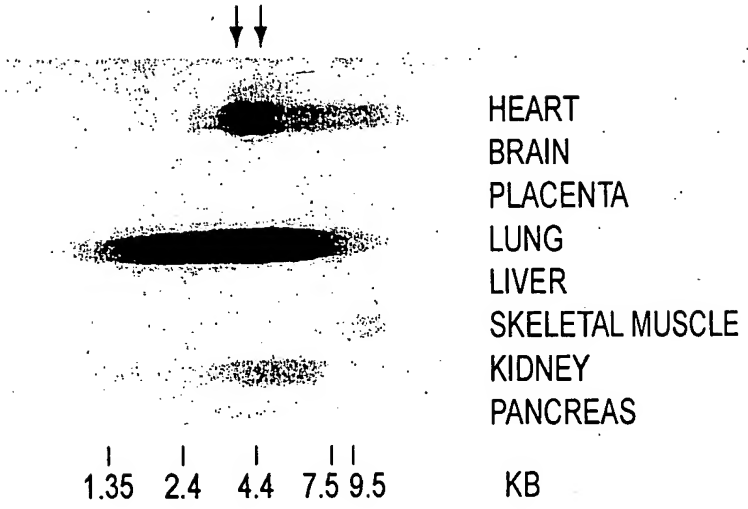
HEART
BRAIN
PLACENTA
LUNG
LIVER
SKELETAL MUSCLE
KIDNEY
PANCREAS
1.35
2.4
4.4
7.5
9.5
KB

FIG. 15